

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:48:33 ; Search time 133.181 Seconds  
(without alignments)  
699.779 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTMGVPTQVLGLLLMLTD.....CQVTHGSGTVEKTVAPTECS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1243	100.0	238	16 US-10-756-125-4
2	1089	87.6	235	9 US-09-747-669-6
3	1089	87.6	235	14 US-10-290-703-6
4	1070.5	86.1	236	9 US-09-758-173-10
5	1070.5	86.1	236	9 US-09-948-4298-10
6	1070.5	86.1	236	13 US-10-124-905-10
7	1070.5	86.1	236	14 US-10-124-807-10
8	1070.5	86.1	236	14 US-10-291-532-10
9	1070.5	86.1	236	18 US-10-986-780-10
10	1067	85.8	233	16 US-10-723-860-27
11	1067	85.8	268	15 US-10-363-616-332
				Sequence 4, Appli
				Sequence 6, Appli
				Sequence 6, Appli
				Sequence 10, Appl
				Sequence 10, Appl
				Sequence 10, Appl
				Sequence 10, Appl
				Sequence 10, Appl
				Sequence 10, Appl
				Sequence 27, Appl
				Sequence 332, App

12	1025	82.5	214	17	US-10-887-231-19	Sequence 19, Appl
13	1020	82.1	214	17	US-10-887-228A-2	Sequence 2, Appli
14	1020	82.1	214	17	US-10-887-231-6	Sequence 6, Appli
15	1020	82.1	214	17	US-10-887-231-17	Sequence 17, Appl
16	1011	81.3	214	16	US-10-128-520-107	Sequence 107, App
17	1009	81.2	214	17	US-10-887-231-37	Sequence 37, Appl
18	1007.5	81.1	213	16	US-10-128-520-112	Sequence 112, App
19	1007	81.0	214	16	US-10-128-520-104	Sequence 104, App
20	1004.5	80.8	213	16	US-10-128-520-105	Sequence 105, App
21	981.5	79.0	234	14	US-10-194-801C-4	Sequence 4, Appli
22	970	78.0	221	13	US-10-001-857-202	Sequence 202, App
23	963.5	77.5	242	14	US-10-225-108A-14	Sequence 14, Appl
24	963.5	77.5	242	15	US-10-461-148-7	Sequence 7, Appli
25	939.5	75.6	234	9	US-09-758-173-2	Sequence 2, Appli
26	939.5	75.6	234	9	US-09-948-4298-2	Sequence 2, Appli
27	939.5	75.6	234	13	US-10-124-905-2	Sequence 2, Appli
28	939.5	75.6	234	14	US-10-124-807-2	Sequence 2, Appli
29	939.5	75.6	234	14	US-10-291-532-2	Sequence 2, Appli
30	939.5	75.6	234	18	US-10-986-780-2	Sequence 2, Appli
31	935	75.2	216	17	US-10-887-231-31	Sequence 31, Appl
32	934	75.1	216	17	US-10-887-231-23	Sequence 23, Appl
33	932	75.0	216	17	US-10-887-231-25	Sequence 25, Appl
34	925	74.4	216	17	US-10-887-228A-10	Sequence 10, Appl
35	925	74.4	216	17	US-10-887-231-10	Sequence 10, Appl
36	923	74.3	216	17	US-10-887-231-29	Sequence 29, Appl
37	923	74.3	216	17	US-10-887-231-33	Sequence 33, Appl
38	922.5	74.2	215	16	US-10-128-520-133	Sequence 133, App
39	921	74.1	216	17	US-10-887-231-39	Sequence 39, Appl
40	919.5	74.0	235	16	US-10-663-244-154	Sequence 154, App
41	918	73.9	216	17	US-10-887-231-21	Sequence 21, Appl
42	916.5	73.7	215	16	US-10-128-520-116	Sequence 116, App
43	915.5	73.7	215	16	US-10-128-520-128	Sequence 128, App
44	915	73.6	216	16	US-10-128-520-119	Sequence 119, App
45	913.5	73.5	215	16	US-10-128-520-117	Sequence 117, App

#### ALIGNMENTS

RESULT 1  
US-10-756-125-4  
; Sequence 4, Application US/10756125  
; Publication No. US20040209244A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Dennis R.  
; APPLICANT: YEE, Sidney  
; TITLE OF INVENTION: ANTI-DENGUE VIRUS ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: 48503-00004  
; CURRENT APPLICATION NUMBER: US/10/756,125  
; PRIOR FILING DATE: 2004-01-12  
; PRIOR APPLICATION NUMBER: 60/443,924  
; PRIOR FILING DATE: 2003-01-31  
; NUMBER OF SEQ IDS NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: light chain  
US-10-756-125-4

Query Match	100.0%	Score 1243;	DB 16;	Length 238;
Best Local Similarity	100.0%	Pred. No. 1.3e-84;		
Matches 238;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	KLTMGVPTQVLGLLLMLTDCQSVLTQPPSASCTPGQRTVISCSTSNIGSTNVWY	60	
DB	1	KLTMGVPTQVLGLLLMLTDCQSVLTQPPSASCTPGQRTVISCSTSNIGSTNVWY	60	
QY	61	QOLCTAPKLIYNDORPSGVDPFSGSKTSASLISGLQSEADYCAAWDDSLN	120	

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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:30:03 ; Search time 37.6114 Seconds  
(without alignments)  
472.369 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KUTMGVPTQVLGILLMLTLD.....CQVTHEGSTVKTVPATPCS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCTUS COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1070.5	86.1	236	3	US-08-487-550-10
2	1070.5	86.1	236	4	US-09-526-098-10
3	1070.5	86.1	236	4	US-09-383-916-10
4	1043	83.9	235	3	US-09-049-672A-12
5	1010.5	81.3	236	3	US-09-049-672A-7
6	986.5	79.4	234	4	US-09-372-425A-4
7	940.5	75.7	235	2	US-08-378-933-12
8	939.5	75.6	234	3	US-08-487-550-2
9	939.5	75.6	234	4	US-09-526-098-2
10	939.5	75.6	234	4	US-09-383-916-2
11	935.5	75.3	235	3	US-09-049-672A-10
12	874.5	70.4	233	3	US-08-523-894-6
13	872	70.2	235	4	US-09-152-060-70
14	869	69.9	235	4	US-09-152-060-88
15	864.5	69.5	240	3	US-09-049-672A-11
16	806.5	64.9	239	3	US-09-828-995B-26
17	792	63.7	238	3	US-08-793-450-6
18	701.5	56.4	216	4	US-09-291-299A-8
19	679	54.6	217	4	US-09-291-299A-7
20	653.5	52.6	216	4	US-09-291-299A-10
21	643.5	51.8	216	4	US-09-291-299A-9
22	631	50.8	229	3	US-08-751-359-22
23	631	50.8	229	3	US-08-907-146-22
24	576	46.3	200	6	5189147-10
25	576	46.3	200	6	5189147-10
26	567	45.6	109	2	US-08-761-277A-51
27	552.5	44.4	111	4	US-09-424-840B-8

28	548	44.1	105	1	US-08-422-101-9	Sequence 9, Appli
29	548	44.1	105	1	US-08-422-091-9	Sequence 9, Appli
30	548	44.1	105	1	US-08-422-092-9	Sequence 9, Appli
31	548	44.1	105	2	US-08-788-800-6	Sequence 6, Appli
32	548	44.1	105	3	US-08-422-093-9	Sequence 9, Appli
33	548	44.1	105	3	US-08-422-112-9	Sequence 9, Appli
34	543	43.7	106	4	US-09-313-942-14	Sequence 14, Appl
35	535	43.0	104	3	US-09-025-769B-170	Sequence 170, App
36	535	43.0	104	4	US-09-490-070A-170	Sequence 170, App
37	535	43.0	104	4	US-09-490-153-170	Sequence 170, App
38	535	43.0	104	4	US-09-490-324-170	Sequence 170, App
39	529.5	42.6	111	1	US-08-264-093-6	Sequence 6, Appli
40	519.5	41.8	235	1	US-08-276-852-153	Sequence 153, App
41	519.5	41.8	235	1	US-08-899-575-153	Sequence 153, App
42	519.5	41.8	235	1	US-08-899-575-153	Sequence 153, App
43	519.5	41.8	235	5	PCT-US95-08743-153	Sequence 153, App
44	518.5	41.7	111	2	US-08-665-202-40	Sequence 40, Appl
45	518.5	41.7	111	4	US-09-315-574-40	Sequence 40, Appl

## ALIGNMENTS

### RESULT 1

US-08-487-550-10  
; Sequence 10, Application US/08487550  
; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 236 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-487-550-10

Query Match 86.1%; Score 1070.5; DB 3; Length 236;

Best Local Similarity 86.4%; Pred. No. 3.1e-75;

Matches 204; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

OY 4 MGVTQVLGILLMLTLDARCSVLTPPSASGTQGVRTISCGSTSNIGSNVNYQQL 63

DB 1 MRVPAQLGLLMLPGARCSVLTPPSVSGAPQKVITISCTGTSNIGGYDLHWYQQL 60

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OM protein - protein search, using sw model

Run on: August 24, 2005, 21:05:54 ; Search time 141.813 Seconds  
(without alignments)  
859.402 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTGVPQVGLLLMLTD.....CQVTHEGSTVEKTVAPTECS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1053.5	84.8	236	2	Q8NEJ1 homo sapien
2	1040	83.7	235	2	Q6GMW6
3	1018	81.9	236	2	Q6GMX4
4	1017	81.8	236	2	Q6GMV7
5	1012.5	81.5	235	2	Q6IN99
6	1004	80.8	237	2	Q6DHW4
7	1000	80.5	236	2	Q6GMX3
8	963	77.5	236	2	Q96B61
9	961	77.3	236	2	Q6IPQ0
10	942.5	75.8	235	2	Q6PIK1
11	939	75.5	236	2	Q6PIQ7
12	933.5	75.1	235	2	Q6FUG0
13	901.5	72.5	233	2	Q6FUA3
14	894.5	72.0	234	2	Q8N355
15	892	71.8	236	2	Q6P5S3
16	886.5	71.3	234	2	Q6GMW3
17	877.5	70.6	235	2	Q6P2J1
18	875.5	70.4	233	2	Q8TBC9
19	868.5	69.9	234	2	Q6GMV8
20	865.5	69.6	233	2	Q8N5F4
21	857.5	69.0	234	2	Q7Z2U7
22	853.5	68.7	234	2	Q6NS95
23	851	68.5	233	2	Q6NS96
24	838.5	67.5	233	2	Q6GMW4
25	821	66.0	233	2	Q96169
26	794	63.9	230	2	Q7Z2U3
27	791	63.6	240	2	Q8WUX3
28	722	58.1	235	2	Q99M11
29	591	47.5	233	2	Q6GNH3
30	590	47.5	231	2	Q6GNB8
31	555	44.7	139	2	Q6PJR7

32	551	44.3	106	2	Q8TCJ5	Q8tcj5 homo sapien
33	548	44.1	105	1	LAC HUMAN	P01842 homo sapien
34	525	42.2	213	1	ILLI HUMAN	P15814 homo sapien
35	510.5	41.1	235	2	Q6GMW0	Q6gmw0 homo sapien
36	510	41.0	236	2	Q6GMW1	Q6gmw1 homo sapien
37	506	40.7	236	2	Q6PIH7	Q6pih7 homo sapien
38	505	40.6	236	2	Q6PIH4	Q6pih4 homo sapien
39	503	40.5	234	2	Q7Z473	Q7z473 homo sapien
40	503	40.5	240	2	Q63ZL4	Q63z14 xenopus lae
41	501	40.3	236	2	Q6PIL8	Q6pil8 homo sapien
42	497	40.0	236	2	Q6GMX0	Q6gmxx0 homo sapien
43	494	39.7	236	2	Q6P5S8	Q6p5s8 homo sapien
44	494	39.7	236	2	Q6PIF5	Q6pit5 homo sapien
45	493	39.7	236	2	Q6GMX8	Q6gmxx8 homo sapien

ALIGNMENTS

RESULT 1  
Q8NEJ1  
ID Q8NEJ1 PRELIMINARY; PRT; 236 AA.  
AC Q8NEJ1  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DB Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.,  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.",  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Srausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC030984; AAH0984.1; -.  
DR HSSP; P01703; 7FAB.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:54:14 ; Search time 30.2124 Seconds  
(without alignments)  
757.952 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KLTMGVPTQVLGLLLMLTD.....CQVTHGSGTVKTVAPTECS 238

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	88.5	233	2 S25752	Ig lambda chain -
2	1091	87.8	234	2 S25757	Ig lambda chain -
3	1068.5	86.0	216	2 A42193	Ig lambda chain (B
4	1067	85.8	233	2 S25744	Ig lambda chain -
5	1063	85.5	235	2 S25750	Ig lambda chain -
6	1053.5	84.8	235	2 S25754	Ig lambda chain -
7	1028.5	82.7	235	2 S05270	Ig lambda chain pr
8	1010.5	81.3	216	2 S03401	Ig lambda chain (K
9	1007.5	81.1	216	2 S25258	Ig lambda chain V
10	1004.5	80.8	232	2 S25742	Ig lambda chain -
11	998	80.3	213	2 S21066	Ig lambda chain V
12	984	79.2	236	2 S25746	Ig lambda chain -
13	969	78.0	217	2 JE0246	Ig lambda chain NI
14	942.5	75.8	235	2 S14675	Ig lambda chain -
15	921.5	74.1	208	2 B49444	Ig lambda chain (N
16	914.5	73.6	235	2 S25759	Ig lambda chain -
17	905.5	72.8	232	2 S25756	Ig lambda chain -
18	895.5	72.0	235	2 S25758	Ig lambda chain -
19	892.5	71.8	231	2 S25738	Ig lambda chain -
20	880.5	70.8	216	2 S69130	Ig lambda chain (D
21	879.5	70.8	233	2 S25751	Ig lambda chain -
22	875	70.4	233	2 S25747	Ig lambda chain -
23	868.5	69.9	216	2 JE0245	Ig lambda chain NI
24	864.5	69.5	233	2 S25741	Ig lambda chain -
25	860.5	69.2	231	2 S25753	Ig lambda chain -
26	857.5	69.0	233	2 S25748	Ig lambda chain -
27	843	67.8	235	2 S25749	Ig lambda chain -
28	841.5	67.7	213	2 JE0247	Ig lambda chain NI
29	841.5	67.7	226	2 S25745	Ig lambda chain -

ALIGNMENTS

RESULT 1

S25752  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25752  
R:Combriato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin 1  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25752  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-233 <COM>  
A:Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 1100; DB 2; Length 233;  
Best Local Similarity 93.9%; Pred. No. 1.7e-61;  
Matches 216; Conservative 3; Mismatches 7; Indels 4; Gaps 2;  
QY 13 LLLLLWLTDA---COSVLTPPSASGTGQRTVITSCSGSTNIGSNVWYQQLPGTAPK 69  
DB 4 LLLTLTHCAGSWAGSVLTQPPSASGTGQRTVITSCSGSSNIGSNVWYQQLPGTAPK 63  
QY 70 LLTYNDQRPQGVDPFRFGSKSGTSGASLAISGLQSEDEADYYCAAWDDSLNG-LFGGGTK 128  
DB 64 LLTYNNQRPQGVDPFRFGSKSGTSGASLAISGLQSEDEADYYCAAWDDSLNGVFGGGTK 123  
QY 129 LTVLQGPKAAPSVTLPFPPSSSELOANKATLVCLISDFYFGAVTVAWKADSSPVKAGVETT 188  
DB 124 LTVLQGPKAAPSVTLPFPPSSSELOANKATLVCLISDFYFGAVTVAWKADSSPVKAGVETT 183  
QY 189 TPKSKNNKYAASSVLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 238  
DB 184 TPKSKNNKYAASSVLSLTPEQWKSHRSYSCQVTHGSGTVKTVAPTECS 233

RESULT 2

S25757  
Ig lambda chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25757  
R:Combriato, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin 1  
A:Reference number: S16439; MUID:91257162; PMID:1904362  
A:Accession: S25757  
A:Status: preliminary; translation not shown

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2005, 20:53:14 ; Search time 144.896 Seconds  
(without alignments)  
635.274 Million cell updates/sec

Title: US-10-756-125-4  
Perfect score: 1243  
Sequence: 1 KUTMGVPTQVLGLLLMLTD.....CQVTHGSEVKTVAPECS 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	238	8	ADRI12638
2	1089	87.6	235	2	AAW88465
3	1070.5	86.1	236	2	AAW63764
4	1070.5	86.1	236	5	AAU11645
5	1070.5	86.1	236	6	AAU11645
6	1067.5	85.9	236	2	AAW01821
7	1067	85.8	233	8	ADQ17211
8	1067	85.8	268	5	ABP62895
9	1063	85.5	236	4	ABG23083
10	1043	83.9	235	4	AAW36214
11	1042	83.8	248	4	ABG26352
12	1027.5	82.7	614	5	ABW06275
13	1027	82.6	234	8	ABW84293
14	1021	82.1	234	8	ABW84291
15	1019.5	82.0	235	8	ABW85086
16	1018.5	81.9	235	8	ABW85069
17	1011	81.3	214	6	ABR01470
18	1010	81.3	236	4	AAW36209
19	1007.5	81.1	213	6	ABR01475
20	1007	81.0	214	6	ABR01467
21	1004.5	80.8	213	6	ABR01468
22	996	80.1	217	2	AAW40533
23	995	80.0	217	2	AAW40533
24	986.5	79.4	234	6	ABG73422
25	981.5	79.0	234	7	AAW39158

26	977	78.6	250	4	ABG19301	Abg19301 Novel hum
27	970	78.0	221	5	ABP52959	Abp52959 Human lun
28	965	77.6	224	8	ABM84279	Abm84279 Human dia
29	964.5	77.6	235	8	ABM84295	Abm84295 Human dia
30	963.5	77.5	235	8	ABM85070	Abm85070 Human dia
31	963.5	77.5	242	6	ABU08021	Abu08021 Monoclonal
32	963.5	77.5	242	7	ADP65786	Adp65786 Human ant
33	963.5	77.5	242	8	ADJ92521	Adj92521 Human ant
34	963	77.5	234	8	ABM85085	Abm85085 Human dia
35	960	77.2	234	8	ABM85071	Abm85071 Human dia
36	959.5	77.2	235	8	ABM84294	Abm84294 Human dia
37	948.5	76.3	249	4	ABG12886	Abg12886 Novel hum
38	944.5	76.0	235	4	AAW64474	AAW64474 Human typ
39	941.5	75.7	251	4	ABG19291	Abg19291 Novel hum
40	940.5	75.7	235	2	AAW01821	AAW01821 Antibody
41	939.5	75.6	234	2	AAW01817	AAW01817 Primatise
42	939.5	75.6	234	2	AAW63760	AAW63760 Macaque p
43	939.5	75.6	234	5	AAU11538	AAU11538 Protein s
44	939.5	75.6	234	6	AAE37359	AAE37359 Monkey 7C
45	938.5	75.5	235	4	AAW64476	AAW64476 Human typ

## ALIGNMENTS

RESULT 1  
ADRI12638  
ID ADRI12638 standard; protein; 238 AA.  
XX  
AC ADRI12638;  
XX  
AC  
XX  
04-NOV-2004 (first entry)  
XX  
Mammalian anti-Dengue virus antibody light chain.  
DE  
virucide; gene therapy; Dengue virus; antibody; diagnosis; heavy chain.  
XX  
Homo sapiens.  
XX  
WO2004067567-A2.  
XX  
12-AUG-2004.  
XX  
30-JAN-2004; 2004WO-EP000896.  
XX  
31-JAN-2003; 2003US-0443924P.  
XX  
(NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS PHARMA GMBH.  
PA (SRI ) SCRIPPS RES INST.  
XX  
Burton DR, Parren PWI, Xee S;  
XX  
WPI; 2004-594168/57.  
DR N-PSDB; ADRI12636.  
XX  
New isolated mammalian anti-Dengue virus antibody useful for diagnosing, preventing or treating Dengue virus infection and its associated diseases.  
XX  
Claim 1; SEQ ID NO 4; 111pp; English.  
XX  
The invention relates to an isolated mammalian anti-Dengue virus antibody. The composition, methods and device are useful for diagnosing, preventing or treating Dengue virus infection and its associated diseases. This sequence corresponds to the anti-Dengue virus antibody light chain.

Sequence 238 AA;

Query Match 100.0%; Score 1243; DB 8; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9.2e-72;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;